

SEQUENCE LISTING

<110> TOMLINSON, Stephen
HOLERS, V. Michael

<120> Complement Receptor 2 Targeted
Complement Modulators

<130> 577712000200

<140> US 10/534,772

<141> 2003-11-13

<150> PCT/US2003/036459

<151> 2003-11-13

<150> US 60/426,676

<151> 2002-11-15

<160> 29

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1041

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 1

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tttcccagg atactgtaat aacgtacaaa tgtgaagaaa gctttgtgaa aattcctggc 120
gagaaggact cagtgatctg ccttaagggc agtcaatggt cagatattga agagttctgc 180
aatcgtagct gcgaggtgcc aacaaggcta aattctgcat ccctcaaaca gccttatatc 240
actcagaatt attttccagt cgggtactgt gtggaatatg agtgccgtcc aggttacaga 300
agagaacctt ctctatcacc aaaactaact tgccttcaga atttaaaatg gtccacagca 360
gtcgaatttt gtaaaaagaa atcatgccct aatccgggag aaatacgaaa tggtcagatt 420
gatgtaccag gtggcatatt atttggtgca accatctcct tctcatgtaa cacagggtac 480
aaattatttg gctcgacttc tagtttttgt cttatttcag gcagctctgt ccagtggagt 540
gacccgttgc cagagtgcag agaaatttat tgtccagcac caccacaaat tgacaatgga 600
ataattcaag gggaacgtga ccattatgga tatagacagt ctgtaacgta tgcattgta 660
aaaggattca ccatgattgg agagcactct atttattgta ctgtgaataa tgatgaagga 720
gagtggagtg gccaccacc tgaatgcaga ggaaaatctc taacttccaa ggtcccacca 780
acagttcaga aacctaccac agtaaatggt ccaactacag aagtctcacc aacttctcag 840
aaaaccacca caaaaaccac cacaccaa atgtcaagcaa cacggagtac acctgtttcc 900
aggacaacca agcattttca tgaacaacc ccaaataaag gaagtggaa cacttcaggt 960
actaccgtc ttctatctgg gcacacgtgt ttcacgttga caggtttgct tgggacgcta 1020
gtaaccatgg gcttgctgac t 1041
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<210> 2

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 2

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Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala Leu Pro Leu Leu Gly
 1          5          10          15
Glu Leu Pro Arg Leu Leu Leu Leu Val Leu Leu Cys Leu Pro Ala Val
          20          25          30
Trp Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu
          35          40          45
Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys
          50          55          60
Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile Cys
65          70          75          80
Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser
          85          90          95
Cys Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr
          100          105          110
Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu Cys
          115          120          125
Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr Cys
          130          135          140
Leu Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys Lys
145          150          155          160
Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val Pro
          165          170          175
Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr Gly
          180          185          190
Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly Ser
          195          200          205
Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr Cys
          210          215          220
Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg Asp
225          230          235          240
His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly Phe
          245          250          255
Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp Glu
          260          265          270
Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu Thr
          275          280          285
Ser Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val Pro
          290          295          300
Thr Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr Thr
305          310          315          320
Thr Pro Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr Thr
          325          330          335
Lys His Phe His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr Ser
          340          345          350
Gly Thr Thr Arg Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly
          355          360          365
Leu Leu Gly Thr Leu Val Thr Met Gly Leu Leu Thr
          370          375          380
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<210> 3

<211> 306

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 3
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gattttgatg cgtgtctcat taccaaagct gggttacaag tgtataacaa gtgttggaag 120
tttgagcatt gcaatttcaa cgacgtcaca acccgcttga gggaaaatga gctaacgtac 180
tactgtcgca agaaggacct gtgtaacttt aacgaacagc ttgaaaatgg tgggacatcc 240
ttatcagaga aaacagttct tctgctgggtg actccatttc tggcagcagc ctggagcctt 300
catccc 306

<210> 4
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 4
Met Gly Ile Gln Gly Gly Ser Val Leu Phe Gly Leu Leu Leu Val Leu
1 5 10 15
Ala Val Phe Cys His Ser Gly His Gln Cys Tyr Asn Cys Pro Asn Pro
20 25 30
Thr Ala Asp Cys Lys Thr Ala Val Asn Cys Ser Ser Asp Phe Asp Ala
35 40 45
Cys Leu Ile Thr Lys Ala Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys
50 55 60
Phe Glu His Cys Asn Phe Asn Asp Val Thr Thr Arg Leu Arg Glu Asn
65 70 75 80
Glu Leu Thr Tyr Tyr Cys Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu
85 90 95
Gln Leu Glu Asn Gly Gly Thr Ser Leu Ser Glu Lys Thr Val Leu Leu
100 105 110
Leu Val Thr Pro Phe Leu Ala Ala Ala Trp Ser Leu His Pro
115 120 125

<210> 5
<211> 1485
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 5
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attgctgttg gtaccgtgat aaggtacagt tgttcaggtc ccttcgcct cattggagaa 120
aaaagtcatt tatgcataac taaagacaaa gtggatggaa cctgggataa acctgctcct 180
aaatgtgaat atttcaataa atattcttct tgccctgagc ccatagtacc aggaggatac 240
aaaattagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaacc 300
aacttctcca tgaacggaaa caagtctgtt tgggtgcaag caaataatat gtgggggccc 360
acacgactac caacctgtgt aagtgttttc cctctcgagt gtccagcact tcctatgatc 420
cacaatggac atcacacaag tgagaatgtt ggctccattg ctccaggatt gtctgtgact 480
tacagctgtg aatctggtta cttgcttgtt ggagaaaaga tcattaactg tttgtcttcg 540
ggaaaatgga gtgctgtccc ccccatatgt gaagaggcac gctgtaaact tctaggacga 600
tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttggtgtaac tgcaaaactt 660
ttctgtgatg aagggtatcg actgcaaggc ccaccttcta gtcggtgtgt aattgctgga 720
cagggagttg cttggaccaa aatgccagta tgtggaggtg ggtcgggtgg cggcggatcc 780
gactgtggcc ttccccaga tgtacctaat gccagccag ctttggaagg ccgtacaagt 840
tttcccgagg atactgtaat aacgtacaaa tgtgaagaaa gctttgtgaa aattcctggc 900

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gagaaggact cagtgatctg ccttaagggc agtcaatggg cagatattga agagttctgc 960
aatcgtagct gcgagggtgcc aacaaggcta aattctgcat ccctcaaaca gccttatatc 1020
actcagaatt attttccagt cgggtactgt gtggaatatg agtgccgtcc aggttacaga 1080
agagaacctt ctctatcacc aaaactaact tgccttcaga atttaaaatg gtccacagca 1140
gtcgaatttt gtaaaaagaa atcatgccct aatccgggag aaatacgaaa tggtcagatt 1200
gatgtaccag gtggcatatt atttggtgca accatctcct tctcatgtaa cacagggtag 1260
aaattatttg gctcgacttc tagtttttgt cttatttcag gcagctctgt ccagtggagt 1320
gacccgttgc cagagtgcag agaaatttat tgtccagcac caccacaaat tgacaatgga 1380
ataattcaag gggaacgtga ccattatgga tatagacagt ctgtaacgta tgcattgta 1440
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<210> 6
<211> 495
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:/note =
        synthetic construct

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<400> 6
Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr
 1           5           10           15
Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser
           20           25           30
Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys
           35           40           45
Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr
           50           55           60
Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr
           65           70           75           80
Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe
           85           90           95
Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys
           100          105          110
Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser
           115          120          125
Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile His Asn Gly His
           130          135          140
His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr
           145          150          155          160
Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn
           165          170          175
Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu
           180          185          190
Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu
           195          200          205
Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu
           210          215          220
Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys Val Ile Ala Gly
           225          230          235          240
Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Gly Gly Gly Ser Gly
           245          250          255
Gly Gly Gly Ser Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln
           260          265          270
Pro Ala Leu Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr
           275          280          285
Tyr Lys Cys Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser
           290          295          300
Val Ile Cys Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys
           305          310          315          320

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Asn	Arg	Ser	Cys	Glu	Val	Pro	Thr	Arg	Leu	Asn	Ser	Ala	Ser	Leu	Lys
				325					330					335	
Gln	Pro	Tyr	Ile	Thr	Gln	Asn	Tyr	Phe	Pro	Val	Gly	Thr	Val	Val	Glu
			340					345					350		
Tyr	Glu	Cys	Arg	Pro	Gly	Tyr	Arg	Arg	Glu	Pro	Ser	Leu	Ser	Pro	Lys
		355					360					365			
Leu	Thr	Cys	Leu	Gln	Asn	Leu	Lys	Trp	Ser	Thr	Ala	Val	Glu	Phe	Cys
	370					375					380				
Lys	Lys	Lys	Ser	Cys	Pro	Asn	Pro	Gly	Glu	Ile	Arg	Asn	Gly	Gln	Ile
	385				390					395					400
Asp	Val	Pro	Gly	Gly	Ile	Leu	Phe	Gly	Ala	Thr	Ile	Ser	Phe	Ser	Cys
			405						410					415	
Asn	Thr	Gly	Tyr	Lys	Leu	Phe	Gly	Ser	Thr	Ser	Ser	Phe	Cys	Leu	Ile
		420						425					430		
Ser	Gly	Ser	Ser	Val	Gln	Trp	Ser	Asp	Pro	Leu	Pro	Glu	Cys	Arg	Glu
	435					440						445			
Ile	Tyr	Cys	Pro	Ala	Pro	Pro	Gln	Ile	Asp	Asn	Gly	Ile	Ile	Gln	Gly
	450					455					460				
Glu	Arg	Asp	His	Tyr	Gly	Tyr	Arg	Gln	Ser	Val	Thr	Tyr	Ala	Cys	Asn
	465			470						475					480
Lys	Gly	Phe	Thr	Met	Ile	Gly	Glu	His	Ser	Ile	Tyr	Cys	Thr	Val	
				485					490					495	

<210> 7

<211> 1002

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 7

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aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataa acctgctcct 180
aaatgtgaat atttcaataa atattcttct tgccctgagc ccatagtacc aggaggatac 240
aaaattagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaacc 300
aacttctcca tgaacggaaa caagtctggt tgggtgtcaag caaataatat gtgggggccg 360
acacgactac caacctgtgt aagtgttttc cctctcgagt gtccagcact tcctatgatc 420
cacaatggac atcacacaag tgagaatggt ggctccattg ctccaggatt gtctgtgact 480
tacagctgtg aatctgggta cttgcttgtt ggagaaaaga tcattaactg tttgtcttcg 540
ggaaaatgga gtgctgtccc cccacatgt gaagaggcac gctgtaaatc tctaggacga 600
tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttggtgtaac tgcaaaacttt 660
ttctgtgatg aagggtatcg actgcaaggc ccaccttcta gtcggtgtgt aattgctgga 720
caggaggttg cttggaccaa aatgccagta tgttcaggag gaggagggtc cctgcagtgc 780
tacaactgtc ctaacccaac tgctgactgc aaaacagccg tcaattgttc atctgatttt 840
gatgcgtgtc tcattaccaa agctgggtta caagtgtata acaagtgttg gaagtttgag 900
cattgcaatt tcaacgacgt cacaaccgcg ttgagggaaa atgagctaac gtactactgc 960
tgcaagaagg acctgtgtaa ctttaacgaa cagcttgaaa at                                     1002

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<210> 8

<211> 334

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 8

Ile	Ser	Cys	Gly	Ser	Pro	Pro	Pro	Ile	Leu	Asn	Gly	Arg	Ile	Ser	Tyr
1				5					10					15	
Tyr	Ser	Thr	Pro	Ile	Ala	Val	Gly	Thr	Val	Ile	Arg	Tyr	Ser	Cys	Ser
			20					25					30		
Gly	Thr	Phe	Arg	Leu	Ile	Gly	Glu	Lys	Ser	Leu	Leu	Cys	Ile	Thr	Lys
		35				40					45				
Asp	Lys	Val	Asp	Gly	Thr	Trp	Asp	Lys	Pro	Ala	Pro	Lys	Cys	Glu	Tyr
	50					55					60				
Phe	Asn	Lys	Tyr	Ser	Ser	Cys	Pro	Glu	Pro	Ile	Val	Pro	Gly	Gly	Tyr
65				70						75				80	
Lys	Ile	Arg	Gly	Ser	Thr	Pro	Tyr	Arg	His	Gly	Asp	Ser	Val	Thr	Phe
				85					90					95	
Ala	Cys	Lys	Thr	Asn	Phe	Ser	Met	Asn	Gly	Asn	Lys	Ser	Val	Trp	Cys
			100					105					110		
Gln	Ala	Asn	Asn	Met	Trp	Gly	Pro	Thr	Arg	Leu	Pro	Thr	Cys	Val	Ser
	115					120						125			
Val	Phe	Pro	Leu	Glu	Cys	Pro	Ala	Leu	Pro	Met	Ile	His	Asn	Gly	His
	130					135					140				
His	Thr	Ser	Glu	Asn	Val	Gly	Ser	Ile	Ala	Pro	Gly	Leu	Ser	Val	Thr
145				150						155				160	
Tyr	Ser	Cys	Glu	Ser	Gly	Tyr	Leu	Leu	Val	Gly	Glu	Lys	Ile	Ile	Asn
				165					170					175	
Cys	Leu	Ser	Ser	Gly	Lys	Trp	Ser	Ala	Val	Pro	Pro	Thr	Cys	Glu	Glu
			180					185					190		
Ala	Arg	Cys	Lys	Ser	Leu	Gly	Arg	Phe	Pro	Asn	Gly	Lys	Val	Lys	Glu
	195					200						205			
Pro	Pro	Ile	Leu	Arg	Val	Gly	Val	Thr	Ala	Asn	Phe	Phe	Cys	Asp	Glu
	210					215						220			
Gly	Tyr	Arg	Leu	Gln	Gly	Pro	Pro	Ser	Ser	Arg	Cys	Val	Ile	Ala	Gly
225				230						235				240	
Gln	Gly	Val	Ala	Trp	Thr	Lys	Met	Pro	Val	Cys	Ser	Gly	Gly	Gly	Gly
				245					250					255	
Ser	Leu	Gln	Cys	Tyr	Asn	Cys	Pro	Asn	Pro	Thr	Ala	Asp	Cys	Lys	Thr
			260					265					270		
Ala	Val	Asn	Cys	Ser	Ser	Asp	Phe	Asp	Ala	Cys	Leu	Ile	Thr	Lys	Ala
	275						280					285			
Gly	Leu	Gln	Val	Tyr	Asn	Lys	Cys	Trp	Lys	Phe	Glu	His	Cys	Asn	Phe
	290					295				300					
Asn	Asp	Val	Thr	Thr	Arg	Leu	Arg	Glu	Asn	Glu	Leu	Thr	Tyr	Tyr	Cys
305					310					315					320
Cys	Lys	Lys	Asp	Leu	Cys	Asn	Phe	Asn	Glu	Gln	Leu	Glu	Asn		
				325					330						

<210> 9

<211> 1554

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 9

gactgtggcc	ttccccaga	tgtacctaat	gccagccag	ctttggaagg	ccgtacaagt	60
tttcccagg	atactgta	aacgtacaaa	tgtgaagaaa	gctttgtgaa	aattcctggc	120
gagaaggact	cagtgatctg	ccttaagggc	agtcaatggt	cagatattga	agagttctgc	180
aatcgtagct	gagaggtgcc	aacaaggcta	aattctgcat	ccctcaaaca	gccttatatc	240
actcagaatt	atcttccagt	cggtactgtt	gtggaatatg	agtgccgtcc	aggttacaga	300
agagaacctt	ctctatcacc	aaaactaact	tgcccttcaga	atttaaaatg	gtccacagca	360

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gtcgaatttt gtaaaaagaa atcatgccct aatccgggag aaatacgaaa tggtcagatt 420
gatgtaccag gtggcatatt atttgggtgca accatctcct tctcatgtaa cacaggggtac 480
aaattatttg gctcgacttc tagtttttgt cttatttcag gcagctctgt ccagtggagt 540
gacccgttgc cagagtgcag agaaatttat tgtccagcac caccacaaat tgacaatgga 600
ataattcaag gggaacgtga ccattatgga tatagacagt ctgtaacgta tgcattgta 660
aaaggattca ccatgattgg agagcactct atttattgta ctgtgaataa tgatgaagga 720
gagtggagtg gccaccacc tgaatgcaga tcctctggtg gcggtggctc gggcggaggt 780
gggtcgggtg gcggcggatc catttcttgt ggctctcctc cgctatcct aaatggccgg 840
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accttccgcc tcattggaga aaaaagtcta ttatgcataa ctaaaagaaa agtggatgga 960
acctgggata aacctgctcc taaatgtgaa tatttcaata aatattcttc ttgccctgag 1020
cccatagtag caggaggata caaaattaga ggctctacac cctacagaca tggtagattct 1080
gtgacatttg cctgtaaaac caacttctcc atgaacggaa acaagtctgt ttggtgtcaa 1140
gcaaataata tgtggggggc gacacgacta ccaacctgtg taagtgtttt ccctctcgag 1200
tgtccagcac ttcctatgat ccacaatgga catcacaaa gtgagaatgt tggctccatt 1260
gctccaggat tgtctgtgac ttacagctgt gaatctggtt acttgcttgt tggagaaaag 1320
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cgctgtaa at ctctaggacg atttcccaat gggaaggtaa aggagcctcc aattctccgg 1440
gttgggtgtaa ctgcaaacct tttctgtgat gaagggtatc gactgcaagg cccaccttct 1500
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<210> 10

<211> 518

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =

synthetic construct

<400> 10

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Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu Glu
 1             5             10             15
Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu
          20          25          30
Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile Cys Leu
          35          40          45
Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser Cys
          50          55          60
Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr Ile
65          70          75          80
Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu Cys Arg
          85          90          95
Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr Cys Leu
          100         105         110
Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys Ser
          115         120         125
Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val Pro Gly
          130         135         140
Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr Gly Tyr
145         150         155         160
Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly Ser Ser
          165         170         175
Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr Cys Pro
          180         185         190
Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg Asp His
          195         200         205
Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly Phe Thr
          210         215         220
Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp Glu Gly

```

225		230		235		240
Glu Trp Ser Gly	Pro Pro Pro Glu Cys Arg	Ser Ser Gly Gly Gly Gly				
	245	250		255		
Ser Gly Gly Gly	Gly Ser Gly Gly Gly Gly	Ser Ile Ser Cys Gly Ser				
	260	265		270		
Pro Pro Pro Ile	Leu Asn Gly Arg Ile Ser Tyr Tyr	Ser Thr Pro Ile				
	275	280		285		
Ala Val Gly Thr	Val Ile Arg Tyr Ser Cys Ser Gly	Thr Phe Arg Leu				
	290	295		300		
Ile Gly Glu Lys	Ser Leu Leu Cys Ile Thr Lys Asp Lys Val Asp Gly					
305	310	315		320		
Thr Trp Asp Lys	Pro Ala Pro Lys Cys Glu Tyr Phe Asn Lys Tyr Ser					
	325	330		335		
Ser Cys Pro Glu	Pro Ile Val Pro Gly Gly Tyr Lys Ile Arg Gly Ser					
	340	345		350		
Thr Pro Tyr Arg	His Gly Asp Ser Val Thr Phe Ala Cys Lys Thr Asn					
	355	360		365		
Phe Ser Met Asn	Gly Asn Lys Ser Val Trp Cys Gln Ala Asn Asn Met					
	370	375		380		
Trp Gly Pro Thr	Arg Leu Pro Thr Cys Val Ser Val Phe Pro Leu Glu					
385	390	395		400		
Cys Pro Ala Leu	Pro Met Ile His Asn Gly His His Thr Ser Glu Asn					
	405	410		415		
Val Gly Ser Ile	Ala Pro Gly Leu Ser Val Thr Tyr Ser Cys Glu Ser					
	420	425		430		
Gly Tyr Leu Leu	Val Gly Glu Lys Ile Ile Asn Cys Leu Ser Ser Gly					
	435	440		445		
Lys Trp Ser Ala	Val Pro Pro Thr Cys Glu Glu Ala Arg Cys Lys Ser					
	450	455		460		
Leu Gly Arg Phe	Pro Asn Gly Lys Val Lys Glu Pro Pro Ile Leu Arg					
465	470	475		480		
Val Gly Val Thr	Ala Asn Phe Phe Cys Asp Glu Gly Tyr Arg Leu Gln					
	485	490		495		
Gly Pro Pro Ser	Ser Arg Cys Val Ile Ala Gly Gln Gly Val Ala Trp					
	500	505		510		
Thr Lys Met Pro	Val Cys					
	515					

<210> 11

<211> 990

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 11

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ccctacagac atggtgattc tgtgacattt gcctgtaaaa ccaacttctc catgaacgga 600
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<210> 12

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 12

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 1          5          10          15
Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly
          20          25          30
Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn
          35          40          45
Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys
          50          55          60
Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn Ser Ser Gly
65          70          75          80
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Ser
          85          90          95
Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr Tyr Ser
          100          105          110
Thr Pro Ile Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser Gly Thr
          115          120          125
Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys Asp Lys
          130          135          140
Val Asp Gly Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr Phe Asn
145          150          155          160
Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr Lys Ile
          165          170          175
Arg Gly Ser Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe Ala Cys
          180          185          190
Lys Thr Asn Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys Gln Ala
          195          200          205
Asn Asn Met Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser Val Phe
          210          215          220
Pro Leu Glu Cys Pro Ala Leu Pro Met Ile His Asn Gly His His Thr
225          230          235          240
Ser Glu Asn Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr Tyr Ser
          245          250          255
Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn Cys Leu
          260          265          270
Ser Ser Gly Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu Ala Arg
          275          280          285
Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu Pro Pro
          290          295          300
Ile Leu Arg Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu Gly Tyr
305          310          315          320
Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys
          325          330

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<210> 13

<211> 5994
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 13
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<210> 14

<211> 2048

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 14

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Leu	Ala	Val	Val	Val	Leu	Leu	Ala	Leu	Pro	Val	Ala	Trp	Gly	Gln	Cys	35	40	45	
Asn	Ala	Gln	Cys	Asn	Ala	Pro	Glu	Trp	Leu	Pro	Phe	Ala	Arg	Pro	Thr	50	55	60	
Asn	Leu	Thr	Asp	Glu	Phe	Glu	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Asn	Tyr	65	70	75	80
Glu	Cys	Arg	Pro	Gly	Tyr	Ser	Gly	Arg	Pro	Phe	Ser	Ile	Ile	Cys	Leu	85	90	95	
Lys	Asn	Ser	Val	Trp	Thr	Gly	Ala	Lys	Asp	Arg	Cys	Arg	Arg	Lys	Ser	100	105	110	
Cys	Arg	Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys	115	120	125	
Gly	Ile	Gln	Phe	Gly	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	130	135	140	
Arg	Leu	Ile	Gly	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr		145	150	155	160
Val	Ile	Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	165	170	175	
Leu	Pro	Pro	Thr	Ile	Thr	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	180	185	190	
Asn	Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	195	200	205	
Gly	Gly	Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	210	215	220	
Thr	Ser	Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	225	230	235	240
Cys	Ile	Ile	Pro	Asn	Lys	Cys	Thr	Pro	Pro	Asn	Val	Glu	Asn	Gly	Ile	245	250	255	
Leu	Val	Ser	Asp	Asn	Arg	Ser	Leu	Phe	Ser	Leu	Asn	Glu	Val	Val	Glu	260	265	270	
Phe	Arg	Cys	Gln	Pro	Gly	Phe	Val	Met	Lys	Gly	Pro	Arg	Arg	Val	Lys	275	280	285	
Cys	Gln	Ala	Leu	Asn	Lys	Trp	Glu	Pro	Glu	Leu	Pro	Ser	Cys	Ser	Arg	290	295	300	
Val	Cys	Gln	Pro	Pro	Pro	Asp	Val	Leu	His	Ala	Glu	Arg	Thr	Gln	Arg	305	310	315	320
Asp	Lys	Asp	Asn	Phe	Ser	Pro	Gly	Gln	Glu	Val	Phe	Tyr	Ser	Cys	Glu	325	330	335	
Pro	Gly	Tyr	Asp	Leu	Arg	Gly	Ala	Ala	Ser	Met	Arg	Cys	Thr	Pro	Gln	340	345	350	
Gly	Asp	Trp	Ser	Pro	Ala	Ala	Pro	Thr	Cys	Glu	Val	Lys	Ser	Cys	Asp	355	360	365	
Asp	Phe	Met	Gly	Gln	Leu	Leu	Asn	Gly	Arg	Val	Leu	Phe	Pro	Val	Asn	370	375	380	
Leu	Gln	Leu	Gly	Ala	Lys	Val	Asp	Phe	Val	Cys	Asp	Glu	Gly	Phe	Gln	385	390	395	400
Leu	Lys	Gly	Ser	Ser	Ala	Ser	Tyr	Cys	Val	Leu	Ala	Gly	Met	Glu	Ser	405	410	415	
Leu	Trp	Asn	Ser	Ser	Val	Pro	Val	Cys	Glu	Gln	Ile	Phe	Cys	Pro	Ser	420	425	430	
Pro	Pro	Val	Ile	Pro	Asn	Gly	Arg	His	Thr	Gly	Lys	Pro	Leu	Glu	Val	435	440	445	
Phe	Pro	Phe	Gly	Lys	Ala	Val	Asn	Tyr	Thr	Cys	Asp	Pro	His	Pro	Asp	450	455	460	
Arg	Gly	Thr	Ser	Phe	Asp	Leu	Ile	Gly	Glu	Ser	Thr	Ile	Arg	Cys	Thr	465	470	475	480
Ser	Asp	Pro	Gln	Gly	Asn	Gly	Val	Trp	Ser	Ser	Pro	Ala	Pro	Arg	Cys				

Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser
 980 985 990
 Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys
 995 1000 1005
 Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val
 1010 1015 1020
 His Val Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys
 1025 1030 1035 1040
 Thr Thr Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu
 1045 1050 1055
 Ser Gly Asn Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg
 1060 1065 1070
 Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser
 1075 1080 1085
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 1090 1095 1100
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 Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val
 1140 1145 1150
 Glu Asn Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn
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 Ser Cys Ser Arg Val Cys Gln Pro Pro Pro Glu Ile Leu His Gly Glu
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 1220 1225 1230
 Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Leu His
 1235 1240 1245
 Cys Thr Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg Cys Ala Val
 1250 1255 1260
 Lys Ser Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly Arg Val Leu
 1265 1270 1275 1280
 Phe Pro Leu Asn Leu Leu Gly Ala Lys Val Ser Phe Val Cys Asp
 1285 1290 1295
 Glu Gly Phe Arg Leu Lys Gly Ser Ser Val Ser His Cys Val Leu Val
 1300 1305 1310
 Gly Met Arg Ser Leu Trp Asn Asn Ser Val Pro Val Cys Glu His Ile
 1315 1320 1325
 Phe Cys Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His Thr Gly Thr
 1330 1335 1340
 Pro Ser Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr Thr Cys Asp
 1345 1350 1355 1360
 Pro His Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly Glu Ser Thr
 1365 1370 1375
 Ile Arg Cys Thr Ser Asp Pro His Gly Asn Gly Val Trp Ser Ser Pro
 1380 1385 1390
 Ala Pro Arg Cys Glu Leu Ser Val Arg Ala Gly His Cys Lys Thr Pro
 1395 1400 1405
 Glu Gln Phe Pro Phe Ala Ser Pro Thr Ile Pro Ile Asn Asp Phe Glu
 1410 1415 1420
 Phe Pro Val Gly Thr Ser Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Phe
 1425 1430 1435 1440
 Gly Lys Met Phe Ser Ile Ser Cys Leu Glu Asn Leu Val Trp Ser Ser
 1445 1450 1455
 Val Glu Asp Asn Cys Arg Arg Lys Ser Cys Gly Pro Pro Pro Glu Pro

1460										1465					1470								
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1475										1480					1485								
Val	Asn	Tyr	Ser	Cys	Asn	Glu	Gly	Phe	Arg	Leu	Ile	Gly	Ser	Pro	Ser								
1490										1495					1500								
Thr	Thr	Cys	Leu	Val	Ser	Gly	Asn	Asn	Val	Thr	Trp	Asp	Lys	Lys	Ala								
1505						1510						1515						1520					
Pro	Ile	Cys	Glu	Ile	Ile	Ser	Cys	Glu	Pro	Pro	Pro	Thr	Ile	Ser	Asn								
1525										1530					1535								
Gly	Asp	Phe	Tyr	Ser	Asn	Asn	Arg	Thr	Ser	Phe	His	Asn	Gly	Thr	Val								
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1585						1590						1595						1600					
Thr	Ala	Pro	Glu	Val	Glu	Asn	Ala	Ile	Arg	Val	Pro	Gly	Asn	Arg	Ser								
1605										1610					1615								
Phe	Phe	Ser	Leu	Thr	Glu	Ile	Ile	Arg	Phe	Arg	Cys	Gln	Pro	Gly	Phe								
1620										1625					1630								
Val	Met	Val	Gly	Ser	His	Thr	Val	Gln	Cys	Gln	Thr	Asn	Gly	Arg	Trp								
1635										1640					1645								
Gly	Pro	Lys	Leu	Pro	His	Cys	Ser	Arg	Val	Cys	Gln	Pro	Pro	Pro	Glu								
1650										1655					1660								
Ile	Leu	His	Gly	Glu	His	Thr	Leu	Ser	His	Gln	Asp	Asn	Phe	Ser	Pro								
1665						1670						1675						1680					
Gly	Gln	Glu	Val	Phe	Tyr	Ser	Cys	Glu	Pro	Ser	Tyr	Asp	Leu	Arg	Gly								
1685										1690					1695								
Ala	Ala	Ser	Leu	His	Cys	Thr	Pro	Gln	Gly	Asp	Trp	Ser	Pro	Glu	Ala								
1700										1705					1710								
Pro	Arg	Cys	Thr	Val	Lys	Ser	Cys	Asp	Asp	Phe	Leu	Gly	Gln	Leu	Pro								
1715										1720					1725								
His	Gly	Arg	Val	Leu	Leu	Pro	Leu	Asn	Leu	Gln	Leu	Gly	Ala	Lys	Val								
1730										1735					1740								
Ser	Phe	Val	Cys	Asp	Glu	Gly	Phe	Arg	Leu	Lys	Gly	Arg	Ser	Ala	Ser								
1745						1750						1755						1760					
His	Cys	Val	Leu	Ala	Gly	Met	Lys	Ala	Leu	Trp	Asn	Ser	Ser	Val	Pro								
1765										1770					1775								
Val	Cys	Glu	Gln	Ile	Phe	Cys	Pro	Asn	Pro	Pro	Ala	Ile	Leu	Asn	Gly								
1780										1785					1790								
Arg	His	Thr	Gly	Thr	Pro	Phe	Gly	Asp	Ile	Pro	Tyr	Gly	Lys	Glu	Ile								
1795										1800					1805								
Ser	Tyr	Ala	Cys	Asp	Thr	His	Pro	Asp	Arg	Gly	Met	Thr	Phe	Asn	Leu								
1810										1815					1820								
Ile	Gly	Glu	Ser	Ser	Ile	Arg	Cys	Thr	Ser	Asp	Pro	Gln	Gly	Asn	Gly								
1825						1830						1835						1840					
Val	Trp	Ser	Ser	Pro	Ala	Pro	Arg	Cys	Glu	Leu	Ser	Val	Pro	Ala	Ala								
1845										1850					1855								
Cys	Pro	His	Pro	Pro	Lys	Ile	Gln	Asn	Gly	His	Tyr	Ile	Gly	Gly	His								
1860										1865					1870								
Val	Ser	Leu	Tyr	Leu	Pro	Gly	Met	Thr	Ile	Ser	Tyr	Thr	Cys	Asp	Pro								
1875										1880					1885								
Gly	Tyr	Leu	Leu	Val	Gly	Lys	Gly	Phe	Ile	Phe	Cys	Thr	Asp	Gln	Gly								
1890										1895					1900								
Ile	Trp	Ser	Gln	Leu	Asp	His	Tyr	Cys	Lys	Glu	Val	Asn	Cys	Ser	Phe								
1905						1910						1915						1920					
Pro	Leu	Phe	Met	Asn	Gly	Ile	Ser	Lys	Glu	Leu	Glu	Met	Lys	Lys	Val								
1925										1930					1935								
Tyr	His	Tyr	Gly	Asp	Tyr	Val	Thr	Leu	Lys	Cys	Glu	Asp	Gly	Tyr	Thr								

1940	1945	1950
Leu Glu Gly Ser Pro Trp Ser Gln Cys Gln Ala Asp Asp Arg Trp Asp		
1955	1960	1965
Pro Pro Leu Ala Lys Cys Thr Ser Arg Ala His Asp Ala Leu Ile Val		
1970	1975	1980
Gly Thr Leu Ser Gly Thr Ile Phe Phe Ile Leu Leu Ile Ile Phe Leu		
1985	1990	1995
Ser Trp Ile Ile Leu Lys His Arg Lys Gly Asn Asn Ala His Glu Asn		2000
2005	2010	2015
Pro Lys Glu Val Ala Ile His Leu His Ser Gln Gly Gly Ser Ser Val		
2020	2025	2030
His Pro Arg Thr Leu Gln Thr Asn Glu Glu Asn Ser Arg Val Leu Pro		
2035	2040	2045

<210> 15
 <211> 1029
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 15
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 gagattggtg aacgagtaga ttataagtgt aaaaaaggat acttctatat acctcctctt 120
 gccacccata ctatttgtga tcggaatcat acatgggtac ctgtctcaga tgacgcctgt 180
 tatagagaaa catgtccata tatacgggat cctttaaatg gccaaagcagt ccctgcaaat 240
 gggacttacg agtttggtta tcagatgcac tttatttgta atgagggtta ttacttaatt 300
 ggtgaagaaa ttctatattg tgaacttaaa ggatcagtag caatttggag cggtaaagccc 360
 ccaatatgtg aaaaggtttt gtgtacacca cctccaaaaa taaaaaatgg aaaacacacc 420
 tttagtgaag tagaagtatt tgagtatctt gatgcagtaa cttatagttg tgatcctgca 480
 cctggaccag atccattttc acttattgga gagagcacga tttattgtgg tgacaattca 540
 gtgtggagtc gtgctgtccc agagtgtaaa gtggtcaaat gtcgatttcc agtagtcgaa 600
 aatggaaaac agatatcagg atttggaaaa aaattttact acaaagcaac agttatgttt 660
 gaatgcgata agggttttta cctcgatggc agcgacacaa ttgtctgtga cagtaacagt 720
 acttgggatc cccagttcc aaagtgtcct aaagtgtcga cttcttccac tacaaaatct 780
 ccagcgtcca gtgctcagg tcctaggcct acttacaagc ctccagtctc aaattatcca 840
 ggatatccta aacctgagga aggaatactt gacagtttgg atgtttgggt cattgctgtg 900
 attgttattg ccatagttgt tggagttgca gtaatttgtg ttgtcccgtg cagatatctt 960
 caaaggagga agaagaaagg cacataccta actgatgaga cccacagaga agtaaaattt 1020
 acttctctc 1029

<210> 16
 <211> 378
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 16
 Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe
 1 5 10 15
 Phe Pro Gly Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe
 20 25 30
 Ser Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile
 35 40 45
 Gly Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys

50						55						60					
Cys	Lys	Lys	Gly	Tyr	Phe	Tyr	Ile	Pro	Pro	Leu	Ala	Thr	His	Thr	Ile		
65					70					75					80		
Cys	Asp	Arg	Asn	His	Thr	Trp	Leu	Pro	Val	Ser	Asp	Asp	Ala	Cys	Tyr		
				85					90					95			
Arg	Glu	Thr	Cys	Pro	Tyr	Ile	Arg	Asp	Pro	Leu	Asn	Gly	Gln	Ala	Val		
			100					105					110				
Pro	Ala	Asn	Gly	Thr	Tyr	Glu	Phe	Gly	Tyr	Gln	Met	His	Phe	Ile	Cys		
		115					120					125					
Asn	Glu	Gly	Tyr	Tyr	Leu	Ile	Gly	Glu	Glu	Ile	Leu	Tyr	Cys	Glu	Leu		
		130				135					140						
Lys	Gly	Ser	Val	Ala	Ile	Trp	Ser	Gly	Lys	Pro	Pro	Ile	Cys	Glu	Lys		
145					150					155					160		
Val	Leu	Cys	Thr	Pro	Pro	Pro	Lys	Ile	Lys	Asn	Gly	Lys	His	Thr	Phe		
				165					170					175			
Ser	Glu	Val	Glu	Val	Phe	Glu	Tyr	Leu	Asp	Ala	Val	Thr	Tyr	Ser	Cys		
			180					185					190				
Asp	Pro	Ala	Pro	Gly	Pro	Asp	Pro	Phe	Ser	Leu	Ile	Gly	Glu	Ser	Thr		
		195					200					205					
Ile	Tyr	Cys	Gly	Asp	Asn	Ser	Val	Trp	Ser	Arg	Ala	Ala	Pro	Glu	Cys		
		210				215					220						
Lys	Val	Val	Lys	Cys	Arg	Phe	Pro	Val	Val	Glu	Asn	Gly	Lys	Gln	Ile		
225					230					235					240		
Ser	Gly	Phe	Gly	Lys	Lys	Phe	Tyr	Tyr	Lys	Ala	Thr	Val	Met	Phe	Glu		
				245					250					255			
Cys	Asp	Lys	Gly	Phe	Tyr	Leu	Asp	Gly	Ser	Asp	Thr	Ile	Val	Cys	Asp		
			260					265					270				
Ser	Asn	Ser	Thr	Trp	Asp	Pro	Pro	Val	Pro	Lys	Cys	Leu	Lys	Val	Ser		
		275				280						285					
Thr	Ser	Ser	Thr	Thr	Lys	Ser	Pro	Ala	Ser	Ser	Ala	Ser	Gly	Pro	Arg		
		290				295					300						
Pro	Thr	Tyr	Lys	Pro	Pro	Val	Ser	Asn	Tyr	Pro	Gly	Tyr	Pro	Lys	Pro		
305					310					315					320		
Glu	Glu	Gly	Ile	Leu	Asp	Ser	Leu	Asp	Val	Trp	Val	Ile	Ala	Val	Ile		
				325					330					335			
Val	Ile	Ala	Ile	Val	Val	Gly	Val	Ala	Val	Ile	Cys	Val	Val	Pro	Tyr		
		340						345				350					
Arg	Tyr	Leu	Gln	Arg	Arg	Lys	Lys	Gly	Thr	Tyr	Leu	Thr	Asp	Glu			
		355				360					365						
Thr	His	Arg	Glu	Val	Lys	Phe	Thr	Ser	Leu								
		370				375											

<210> 17

<211> 440

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 17

Met	Glu	Val	Ser	Ser	Arg	Ser	Ser	Glu	Pro	Leu	Asp	Pro	Val	Trp	Leu		
1			5					10					15				
Leu	Val	Ala	Phe	Gly	Arg	Gly	Gly	Val	Lys	Leu	Glu	Val	Leu	Leu	Leu		
		20					25					30					
Phe	Leu	Leu	Pro	Phe	Thr	Leu	Gly	His	Cys	Pro	Ala	Pro	Ser	Gln	Leu		
		35				40					45						
Pro	Ser	Ala	Lys	Pro	Ile	Asn	Leu	Thr	Asp	Glu	Ser	Met	Phe	Pro	Ile		
		50				55					60						

Gly	Thr	Tyr	Leu	Leu	Tyr	Glu	Cys	Leu	Pro	Gly	Tyr	Ile	Lys	Arg	Gln	65	70	75	80
Phe	Ser	Ile	Thr	Cys	Lys	Gln	Asp	Ser	Thr	Trp	Thr	Ser	Ala	Glu	Asp	85	90	95	
Lys	Cys	Ile	Arg	Lys	Gln	Cys	Lys	Thr	Pro	Ser	Asp	Pro	Glu	Asn	Gly	100	105	110	
Leu	Val	His	Val	His	Thr	Gly	Ile	Gln	Phe	Gly	Ser	Arg	Ile	Asn	Tyr	115	120	125	
Thr	Cys	Asn	Gln	Gly	Tyr	Arg	Leu	Ile	Gly	Ser	Ser	Ala	Val	Cys		130	135	140	
Val	Ile	Thr	Asp	Gln	Ser	Val	Asp	Trp	Asp	Thr	Glu	Ala	Pro	Ile	Cys	145	150	155	160
Glu	Trp	Ile	Pro	Cys	Glu	Ile	Pro	Pro	Gly	Ile	Pro	Asn	Gly	Asp	Phe	165	170	175	
Phe	Ser	Ser	Thr	Arg	Glu	Asp	Phe	His	Tyr	Gly	Met	Val	Val	Thr	Tyr	180	185	190	
Arg	Cys	Asn	Thr	Asp	Ala	Arg	Gly	Lys	Ala	Leu	Phe	Asn	Leu	Val	Gly	195	200	205	
Glu	Pro	Ser	Leu	Tyr	Cys	Thr	Ser	Asn	Asp	Gly	Glu	Ile	Gly	Val	Trp	210	215	220	
Ser	Gly	Pro	Pro	Pro	Gln	Cys	Ile	Glu	Leu	Asn	Lys	Cys	Thr	Pro	Pro	225	230	235	240
Pro	Tyr	Val	Glu	Asn	Ala	Val	Met	Leu	Ser	Glu	Asn	Arg	Ser	Leu	Phe	245	250	255	
Ser	Leu	Arg	Asp	Ile	Val	Glu	Phe	Arg	Cys	His	Pro	Gly	Phe	Ile	Met	260	265	270	
Lys	Gly	Ala	Ser	Ser	Val	His	Cys	Gln	Ser	Leu	Asn	Lys	Trp	Glu	Pro	275	280	285	
Glu	Leu	Pro	Ser	Cys	Phe	Lys	Gly	Val	Ile	Cys	Arg	Leu	Pro	Gln	Glu	290	295	300	
Met	Ser	Gly	Phe	Gln	Lys	Gly	Leu	Gly	Met	Lys	Lys	Glu	Tyr	Tyr	Tyr	305	310	315	320
Gly	Glu	Asn	Val	Thr	Leu	Glu	Cys	Glu	Asp	Gly	Tyr	Thr	Leu	Glu	Gly	325	330	335	
Ser	Ser	Gln	Ser	Gln	Cys	Gln	Ser	Asp	Gly	Ser	Trp	Asn	Pro	Leu	Leu	340	345	350	
Ala	Lys	Cys	Val	Ser	Arg	Ser	Ile	Ser	Gly	Leu	Ile	Val	Gly	Ile	Phe	355	360	365	
Ile	Gly	Ile	Ile	Val	Phe	Ile	Leu	Val	Ile	Ile	Val	Phe	Ile	Trp	Met	370	375	380	
Ile	Leu	Lys	Tyr	Lys	Lys	Arg	Asn	Thr	Thr	Asp	Glu	Lys	Tyr	Lys	Glu	385	390	395	400
Val	Gly	Ile	His	Leu	Asn	Tyr	Lys	Glu	Asp	Ser	Cys	Val	Arg	Leu	Gln	405	410	415	
Ser	Leu	Leu	Thr	Ser	Gln	Glu	Asn	Ser	Ser	Thr	Thr	Ser	Pro	Ala	Arg	420	425	430	
Asn	Ser	Leu	Thr	Gln	Glu	Val	Ser									435	440		

<210> 18

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 18

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

1				5					10					15			
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro		
			20					25					30				
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val		
		35					40					45					
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val		
		50				55					60						
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln		
65					70					75					80		
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln		
				85					90					95			
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala		
			100					105					110				
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro		
		115					120					125					
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr		
		130				135					140						
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser		
145					150					155					160		
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr		
			165						170					175			
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Pro	Phe	Phe	Leu	Tyr		
		180					185						190				
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe		
		195				200						205					
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys		
		210				215					220						
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys										
225					230												

<210> 19

<211> 454.

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 19

Gly	Ser	Ala	Ser	Ala	Pro	Thr	Leu	Phe	Pro	Leu	Val	Ser	Cys	Glu	Asn		
1				5				10					15				
Ser	Pro	Ser	Asp	Thr	Ser	Ser	Val	Ala	Val	Gly	Cys	Leu	Ala	Gln	Asp		
		20					25					30					
Phe	Leu	Pro	Asp	Ser	Ile	Thr	Phe	Ser	Trp	Lys	Tyr	Lys	Asn	Asn	Ser		
		35				40					45						
Asp	Ile	Ser	Ser	Thr	Arg	Gly	Phe	Pro	Ser	Val	Leu	Arg	Gly	Gly	Lys		
		50				55				60							
Tyr	Ala	Ala	Thr	Ser	Gln	Val	Leu	Leu	Pro	Ser	Lys	Asp	Val	Met	Gln		
65					70					75					80		
Gly	Thr	Asp	Glu	His	Val	Val	Cys	Lys	Val	Gln	His	Pro	Asn	Gly	Asn		
				85					90					95			
Lys	Glu	Lys	Asn	Val	Pro	Leu	Pro	Val	Ile	Ala	Glu	Leu	Pro	Pro	Lys		
			100				105						110				
Val	Ser	Val	Phe	Val	Pro	Pro	Arg	Asp	Gly	Phe	Phe	Gly	Asn	Pro	Arg		
		115					120					125					
Ser	Lys	Ser	Lys	Leu	Ile	Cys	Gln	Ala	Thr	Gly	Phe	Ser	Pro	Arg	Gln		
		130				135					140						
Ile	Gln	Val	Ser	Trp	Leu	Arg	Glu	Gly	Lys	Gln	Val	Gly	Ser	Gly	Val		
145					150					155					160		

Thr	Thr	Asp	Gln	Val	Gln	Ala	Glu	Ala	Lys	Glu	Ser	Gly	Pro	Thr	Thr		
			165						170					175			
Tyr	Lys	Val	Thr	Ser	Thr	Leu	Thr	Ile	Lys	Glu	Ser	Asp	Trp	Leu	Ser		
			180					185					190				
Gln	Ser	Met	Phe	Thr	Cys	Arg	Val	Asp	His	Arg	Gly	Leu	Thr	Phe	Gln		
		195					200					205					
Gln	Asn	Ala	Ser	Ser	Met	Cys	Val	Pro	Asp	Gln	Asp	Thr	Ala	Ile	Arg		
		210				215					220						
Val	Phe	Ala	Ile	Pro	Pro	Ser	Phe	Ala	Ser	Ile	Phe	Leu	Thr	Lys	Ser		
225					230					235					240		
Thr	Lys	Leu	Thr	Cys	Leu	Val	Thr	Asp	Leu	Thr	Thr	Tyr	Asp	Ser	Val		
			245						250					255			
Thr	Ile	Ser	Trp	Thr	Arg	Gln	Asn	Gly	Glu	Ala	Val	Lys	Thr	His	Thr		
			260					265					270				
Asn	Ile	Ser	Glu	Ser	His	Pro	Asn	Ala	Thr	Phe	Ser	Ala	Val	Gly	Glu		
		275					280					285					
Ala	Ser	Ile	Cys	Glu	Asp	Asp	Trp	Asn	Ser	Gly	Glu	Arg	Phe	Thr	Cys		
		290				295					300						
Thr	Val	Thr	His	Thr	Asp	Leu	Pro	Ser	Pro	Leu	Lys	Gln	Thr	Ile	Ser		
305					310					315					320		
Arg	Pro	Lys	Gly	Val	Ala	Leu	His	Arg	Pro	Asp	Val	Tyr	Leu	Leu	Pro		
			325						330				335				
Pro	Ala	Arg	Glu	Gln	Leu	Asn	Leu	Arg	Glu	Ser	Ala	Thr	Ile	Thr	Cys		
			340					345					350				
Leu	Val	Thr	Gly	Phe	Ser	Pro	Ala	Asp	Val	Phe	Val	Gln	Trp	Met	Gln		
		355					360					365					
Arg	Gly	Gln	Pro	Leu	Ser	Pro	Glu	Lys	Tyr	Val	Thr	Ser	Ala	Pro	Met		
		370				375					380						
Pro	Glu	Pro	Gln	Ala	Pro	Gly	Arg	Tyr	Phe	Ala	His	Ser	Ile	Leu	Thr		
385					390					395					400		
Val	Ser	Glu	Glu	Glu	Trp	Asn	Thr	Gly	Glu	Thr	Tyr	Thr	Cys	Val	Val		
			405						410				415				
Ala	His	Glu	Ala	Leu	Pro	Asn	Arg	Val	Thr	Glu	Arg	Thr	Val	Asp	Lys		
			420					425				430					
Ser	Thr	Gly	Lys	Pro	Thr	Leu	Tyr	Asn	Val	Ser	Leu	Val	Met	Ser	Asp		
		435					440					445					
Thr	Ala	Gly	Thr	Cys	Tyr												
			450														

<210> 20

<211> 1530

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 20

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atttcttggtg gctctcctcc gcctatccta aatggccgga ttagttatta ttctaccccc 120
attgctgttg gtaccgtgat aaggtacagt tggtcaggtc cctccgcct cattggagaa 180
aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataa acctgctcct 240
aaatgtgaat atttcaataa atattcttct tgccctgagc ccatagtacc aggaggatac 300
aaaattagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaacc 360
aacttctcca tgaacggaaa caagtctgtt tgggtcaag caaataatat gtgggggcgcg 420
acacgactac caacctgtgt aagtgttttc cctctcaggt gtccagcact tcctatgac 480
cacaatggac atcacacaag tgagaatggt ggctccattg ctccaggatt gtctgtgact 540
tacagctgtg aatctggtta cttgcttgtt ggagaaaaga tcattaactg tttgtcttcg 600
ggaaaatgga gtgctgtccc ccccatgtgt gaagaggcac gctgtaaatc tctaggacga 660

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tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttggtgtaac tgcaaacttt 720
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cagggaattg cttggaccaaa aatgccagta tgtgaagaaa ttttttgccc actgcgcccg 840
cagtctagag acaaaactca cacatgccca ccgtgccag cacctgaact cctgggggga 900
ccgtcagtct tctcttcccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 960
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 1020
tacgtggacg gcgtggaggt gcataatgcc aagacaaaagc cgcgggagga gcagtacaac 1080
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1140
gagtacaagt gcaagggtctc caacaaagcc ctcccagtc ccatcgagaa aaccatctcc 1200
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag 1260
atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1320
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1380
ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1440
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1500
cagaagagcc tctccctgtc cccgggtaaa 1530

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<210> 21

<211> 510

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 21

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Met Gly Ala Ala Gly Leu Leu Gly Val Phe Leu Ala Leu Val Ala Pro
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Gly Val Leu Gly Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly
          20          25          30
Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg
          35          40          45
Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu
          50          55          60
Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro
65          70          75          80
Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val
          85          90          95
Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp
          100          105          110
Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys
          115          120          125
Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro
          130          135          140
Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile
145          150          155          160

His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly
          165          170          175
Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu
          180          185          190
Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro
          195          200          205
Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly
          210          215          220
Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe
225          230          235          240
Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys
          245          250          255
Val Ile Ala Gly Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu
          260          265          270

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Glu Ile Phe Cys Pro Leu Arg Pro Gln Ser Arg Asp Lys Thr His Thr
 275 280 285
 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 290 295 300
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 305 310 315 320
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 325 330 335
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 340 345 350
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 355 360 365
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 370 375 380
 Lys Val Ser Asn Lys Ala Leu Pro Val Pro Ile Glu Lys Thr Ile Ser
 385 390 395 400
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 405 410 415
 Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 420 425 430
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 435 440 445
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 450 455 460
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 465 470 475 480
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 485 490 495
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 500 505 510

<210> 22

<211> 233

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 22

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 Pro Gly Asn Ile Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
 20 25 30
 Pro Lys Asp Ala Leu Met Ile Ser Leu Thr Pro Lys Val Thr Cys Val
 35 40 45
 Val Val Asp Val Ser Glu Asp Asp Pro Asp Val His Val Ser Trp Phe
 50 55 60
 Val Asp Asn Lys Glu Val His Thr Ala Trp Thr Gln Pro Arg Glu Ala
 65 70 75 80
 Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Ala Leu Pro Ile Gln His
 85 90 95
 Gln Asp Trp Met Arg Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
 100 105 110
 Ala Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Arg
 115 120 125
 Ala Gln Thr Pro Gln Val Tyr Thr Ile Pro Pro Pro Arg Glu Gln Met
 130 135 140
 Ser Lys Lys Lys Val Ser Leu Thr Cys Leu Val Thr Asn Phe Phe Ser

145		150		155		160									
Glu	Ala	Ile	Ser	Val	Glu	Trp	Glu	Arg	Asn	Gly	Glu	Leu	Glu	Gln	Asp
		165							170					175	
Tyr	Lys	Asn	Thr	Pro	Pro	Ile	Leu	Asp	Ser	Asp	Gly	Thr	Tyr	Phe	Leu
		180						185					190		
Tyr	Ser	Lys	Leu	Thr	Val	Asp	Thr	Asp	Ser	Trp	Leu	Gln	Gly	Glu	Ile
		195				200					205				
Phe	Thr	Cys	Ser	Val	Val	His	Glu	Ala	Leu	His	Asn	His	His	Thr	Gln
	210					215					220				
Lys	Asn	Leu	Ser	Arg	Ser	Pro	Gly	Lys							
225					230										

<210> 23
 <211> 4860
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 23
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 cggaagcaga aaaccttggt ccaaaccaga gtagatatga atccagcagg aggcattgctt 180
 gtcactccaa ctatagagat tccagcaaaa gaagttagta cggactccag gcaaaatcaa 240
 tatgtggttg tgcaagtaac tggctctcaa gtgagattgg aaaaggtggt tctcctttct 300
 taccagagta gctttctggt tatccagaca gataaaggca tctatacacc aggtctcca 360
 gtactctatc gtgttttttc tatggatcac aacacaagca agatgaacaa aactgtgatt 420
 gttgagtttc agactccaga aggcatctct gtcagttcta attcagttga cctaaacttc 480
 ttctggcctt acaatttacc agacctgtgc agtttgggga cttggaggat tgtggccaaa 540
 tatgaacatt cccagagaa ttatactgca tattttgatg tcaggaaata tgtgttgcca 600
 agctttgaag tccgtctgca accatcagag aagttttttt acattgacgg caatgaaaat 660
 ttccacgtgt ctatcactgc aaggctactg tatggagagg aagtggagg tgtggccttt 720
 gtcctctttg gagtgaatat agatgatgct aaaaagagta ttccagactc actcacgaga 780
 attccgatta ttgatggaga tgggaaagca aactaaaaa gagatacatt ccgttctcga 840
 tttccaaatc tcaatgagct tgttgggcat actctgtatg catctgtaac agtcatgaca 900
 gaatcaggca gtgattggt agtgactgag caaagcgga ttcattattgt ggcattctcc 960
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 gcctttcatt ctatgggaac cactttgagt gatgggactg ctaagctcat cctgaacata 1140
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 gaacgccagg caacaaagtc catgacagcc atagcctacc aaaccaggg aggatctgga 1260
 aactatcttc atgtagccat tacatctaca gagattaagc ccggagataa cttacctgtc 1320
 aatttcaatg tgaagggcaa tgcaaattca ctgaagcaga tcaaatattt cacatactc 1380
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 tactaccaag tgggaaacaa cgaaattgtg gctgattctg tctgggtgga tgtgaaggat 1560
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 accgaggagc ctaacagtca agggatttca agcaagacaa tgtcttttta tctgagggat 2280

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aagaacacat ggattgagag atggccacat gaagacgaat gtcaggaaga agaattccaa 4800
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<210> 24

<211> 1620

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 24

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Glu Gln Ile Leu Val Glu Ala His Gly Asp Ser Thr Pro Lys Gln Leu
20           25           30
Asp Ile Phe Val His Asp Phe Pro Arg Lys Gln Lys Thr Leu Phe Gln
35           40           45

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Thr	Arg	Val	Asp	Met	Asn	Pro	Ala	Gly	Gly	Met	Leu	Val	Thr	Pro	Thr
50						55					60				
Ile	Glu	Ile	Pro	Ala	Lys	Glu	Val	Ser	Thr	Asp	Ser	Arg	Gln	Asn	Gln
65					70					75					80
Tyr	Val	Val	Val	Gln	Val	Thr	Gly	Pro	Gln	Val	Arg	Leu	Glu	Lys	Val
				85					90					95	
Val	Leu	Leu	Ser	Tyr	Gln	Ser	Ser	Phe	Leu	Phe	Ile	Gln	Thr	Asp	Lys
			100					105					110		
Gly	Ile	Tyr	Thr	Pro	Gly	Ser	Pro	Val	Leu	Tyr	Arg	Val	Phe	Ser	Met
		115					120					125			
Asp	His	Asn	Thr	Ser	Lys	Met	Asn	Lys	Thr	Val	Ile	Val	Glu	Phe	Gln
		130				135					140				
Thr	Pro	Glu	Gly	Ile	Leu	Val	Ser	Ser	Asn	Ser	Val	Asp	Leu	Asn	Phe
145					150					155					160
Phe	Trp	Pro	Tyr	Asn	Leu	Pro	Asp	Leu	Val	Ser	Leu	Gly	Thr	Trp	Arg
				165					170					175	
Ile	Val	Ala	Lys	Tyr	Glu	His	Ser	Pro	Glu	Asn	Tyr	Thr	Ala	Tyr	Phe
			180					185					190		
Asp	Val	Arg	Lys	Tyr	Val	Leu	Pro	Ser	Phe	Glu	Val	Arg	Leu	Gln	Pro
		195					200					205			
Ser	Glu	Lys	Phe	Phe	Tyr	Ile	Asp	Gly	Asn	Glu	Asn	Phe	His	Val	Ser
		210				215					220				
Ile	Thr	Ala	Arg	Tyr	Leu	Tyr	Gly	Glu	Glu	Val	Glu	Gly	Val	Ala	Phe
225					230					235					240
Val	Leu	Phe	Gly	Val	Lys	Ile	Asp	Asp	Ala	Lys	Lys	Ser	Ile	Pro	Asp
				245					250					255	
Ser	Leu	Thr	Arg	Ile	Pro	Ile	Ile	Asp	Gly	Asp	Gly	Lys	Ala	Thr	Leu
			260					265					270		
Lys	Arg	Asp	Thr	Phe	Arg	Ser	Arg	Phe	Pro	Asn	Leu	Asn	Glu	Leu	Val
		275					280					285			
Gly	His	Thr	Leu	Tyr	Ala	Ser	Val	Thr	Val	Met	Thr	Glu	Ser	Gly	Ser
		290				295					300				
Asp	Met	Val	Val	Thr	Glu	Gln	Ser	Gly	Ile	His	Ile	Val	Ala	Ser	Pro
305					310					315					320
Tyr	Gln	Ile	His	Phe	Thr	Lys	Thr	Pro	Lys	Tyr	Phe	Lys	Pro	Gly	Met
				325					330					335	
Pro	Tyr	Glu	Leu	Thr	Val	Tyr	Val	Thr	Asn	Pro	Asp	Gly	Ser	Pro	Ala
			340					345					350		
Ala	His	Val	Pro	Val	Val	Ser	Glu	Ala	Phe	His	Ser	Met	Gly	Thr	Thr
		355					360					365			
Leu	Ser	Asp	Gly	Thr	Ala	Lys	Leu	Ile	Leu	Asn	Ile	Pro	Leu	Asn	Ala
		370				375					380				
Gln	Ser	Leu	Pro	Ile	Thr	Val	Arg	Thr	Asn	His	Gly	Asp	Leu	Pro	Arg
385					390					395					400
Glu	Arg	Gln	Ala	Thr	Lys	Ser	Met	Thr	Ala	Ile	Ala	Tyr	Gln	Thr	Gln
				405					410					415	
Gly	Gly	Ser	Gly	Asn	Tyr	Leu	His	Val	Ala	Ile	Thr	Ser	Thr	Glu	Ile
			420					425					430		
Lys	Pro	Gly	Asp	Asn	Leu	Pro	Val	Asn	Phe	Asn	Val	Lys	Gly	Asn	Ala
		435					440					445			
Asn	Ser	Leu	Lys	Gln	Ile	Lys	Tyr	Phe	Thr	Tyr	Leu	Ile	Leu	Asn	Lys
		450				455					460				
Gly	Lys	Ile	Phe	Lys	Val	Gly	Arg	Gln	Pro	Arg	Arg	Asp	Gly	Gln	Asn
465					470					475					480
Leu	Val	Thr	Met	Asn	Leu	His	Ile	Thr	Pro	Asp	Leu	Ile	Pro	Ser	Phe
				485					490					495	
Arg	Phe	Val	Ala	Tyr	Tyr	Gln	Val	Gly	Asn	Asn	Glu	Ile	Val	Ala	Asp
			500					505					510		
Ser	Val	Trp	Val	Asp	Val	Lys	Asp	Thr	Cys	Met	Gly	Thr	Leu	Val	Val
		515					520					525			
Lys	Gly	Asp	Asn	Leu	Ile	Gln	Met	Pro	Gly	Ala	Ala	Met	Lys	Ile	Lys

530					535					540					
Leu	Glu	Gly	Asp	Pro	Gly	Ala	Arg	Val	Gly	Leu	Val	Ala	Val	Asp	Lys
545					550					555					560
Ala	Val	Tyr	Val	Leu	Asn	Asp	Lys	Tyr	Lys	Ile	Ser	Gln	Ala	Lys	Ile
				565					570						575
Trp	Asp	Thr	Ile	Glu	Lys	Ser	Asp	Phe	Gly	Cys	Thr	Ala	Gly	Ser	Gly
			580					585					590		
Gln	Asn	Asn	Leu	Gly	Val	Phe	Glu	Asp	Ala	Gly	Leu	Ala	Leu	Thr	Thr
	595					600					605				
Ser	Thr	Asn	Leu	Asn	Thr	Lys	Gln	Arg	Ser	Ala	Ala	Lys	Cys	Pro	Gln
	610					615					620				
Pro	Ala	Asn	Arg	Arg	Arg	Arg	Ser	Ser	Val	Leu	Leu	Leu	Asp	Ser	Asn
625				630					635						640
Ala	Ser	Lys	Ala	Ala	Glu	Phe	Gln	Asp	Gln	Asp	Leu	Arg	Lys	Cys	Cys
			645						650					655	
Glu	Asp	Val	Met	His	Glu	Asn	Pro	Met	Gly	Tyr	Thr	Cys	Glu	Lys	Arg
	660							665					670		
Ala	Lys	Tyr	Ile	Gln	Glu	Gly	Asp	Ala	Cys	Lys	Ala	Ala	Phe	Leu	Glu
	675					680					685				
Cys	Cys	Arg	Tyr	Ile	Lys	Gly	Val	Arg	Asp	Glu	Asn	Gln	Arg	Glu	Ser
	690				695						700				
Glu	Leu	Phe	Leu	Ala	Arg	Asp	Asp	Asn	Glu	Asp	Gly	Phe	Ile	Ala	Asp
705				710					715						720
Ser	Asp	Ile	Ile	Ser	Arg	Ser	Asp	Phe	Pro	Lys	Ser	Trp	Leu	Trp	Leu
			725						730					735	
Thr	Lys	Asp	Leu	Thr	Glu	Glu	Pro	Asn	Ser	Gln	Gly	Ile	Ser	Ser	Lys
	740							745					750		
Thr	Met	Ser	Phe	Tyr	Leu	Arg	Asp	Ser	Ile	Thr	Thr	Trp	Val	Val	Leu
	755					760						765			
Ala	Val	Ser	Phe	Thr	Pro	Thr	Lys	Gly	Ile	Cys	Val	Ala	Glu	Pro	Tyr
	770				775						780				
Glu	Ile	Arg	Val	Met	Lys	Val	Phe	Phe	Ile	Asp	Leu	Gln	Met	Pro	Tyr
785				790					795						800
Ser	Val	Val	Lys	Asn	Glu	Gln	Val	Glu	Ile	Arg	Ala	Ile	Leu	His	Asn
			805						810					815	
Tyr	Val	Asn	Glu	Asp	Ile	Tyr	Val	Arg	Val	Glu	Leu	Leu	Tyr	Asn	Pro
	820							825					830		
Ala	Phe	Cys	Ser	Ala	Ser	Thr	Lys	Gly	Gln	Arg	Tyr	Arg	Gln	Gln	Phe
	835						840					845			
Pro	Ile	Lys	Ala	Leu	Ser	Ser	Arg	Ala	Val	Pro	Phe	Val	Ile	Val	Pro
	850				855						860				
Leu	Glu	Gln	Gly	Leu	His	Asp	Val	Glu	Ile	Lys	Ala	Ser	Val	Gln	Glu
865				870					875						880
Ala	Leu	Trp	Ser	Asp	Gly	Val	Arg	Lys	Lys	Leu	Lys	Val	Val	Pro	Glu
			885						890					895	
Gly	Val	Gln	Lys	Ser	Ile	Val	Thr	Ile	Val	Lys	Leu	Asp	Pro	Arg	Ala
	900							905					910		
Lys	Gly	Val	Gly	Gly	Thr	Gln	Leu	Glu	Val	Ile	Lys	Ala	Arg	Lys	Leu
	915					920						925			
Asp	Asp	Arg	Val	Pro	Asp	Thr	Glu	Ile	Glu	Thr	Lys	Ile	Ile	Ile	Gln
	930					935					940				
Gly	Asp	Pro	Val	Ala	Gln	Ile	Ile	Glu	Asn	Ser	Ile	Asp	Gly	Ser	Lys
945				950					955						960
Leu	Asn	His	Leu	Ile	Ile	Thr	Pro	Ser	Gly	Cys	Gly	Glu	Gln	Asn	Met
			965						970					975	
Ile	Arg	Met	Ala	Ala	Pro	Val	Ile	Ala	Thr	Tyr	Tyr	Leu	Asp	Thr	Thr
	980							985					990		
Glu	Gln	Trp	Glu	Thr	Leu	Gly	Ile	Asn	Arg	Arg	Thr	Glu	Ala	Val	Asn
	995					1000						1005			
Gln	Ile	Val	Thr	Gly	Tyr	Ala	Gln	Gln	Met	Val	Tyr	Lys	Lys	Ala	Asp

1010	1015	1020
His Ser Tyr Ala Ala Phe Thr Asn Arg Ala Ser Ser Ser Trp Leu Thr		
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Ala Tyr Val Val Lys Val Phe Ala Met Ala Ala Lys Met Val Ala Gly		1040
	1045	1050
Ile Ser His Glu Ile Ile Cys Gly Gly Val Arg Trp Leu Ile Leu Asn		1055
	1060	1065
Arg Gln Gln Pro Asp Gly Ala Phe Lys Glu Asn Ala Pro Val Leu Ser		1070
	1075	1080
Gly Thr Met Gln Gly Gly Ile Gln Gly Ala Glu Glu Glu Val Tyr Leu		1085
	1090	1095
Thr Ala Phe Ile Leu Val Ala Leu Leu Glu Ser Lys Thr Ile Cys Asn		1100
1105	1110	1115
Asp Tyr Val Asn Ser Leu Asp Ser Ser Ile Lys Lys Ala Thr Asn Tyr		1120
	1125	1130
Leu Leu Lys Lys Tyr Glu Lys Leu Gln Arg Pro Tyr Thr Thr Ala Leu		1135
	1140	1145
Thr Ala Tyr Ala Leu Ala Ala Ala Asp Gln Leu Asn Asp Arg Val		1150
	1155	1160
Leu Met Ala Ala Ser Thr Gly Arg Asp His Trp Glu Glu Tyr Asn Ala		1165
1170	1175	1180
His Thr His Asn Ile Glu Gly Thr Ser Tyr Ala Leu Leu Ala Leu Leu		1185
1185	1190	1195
Lys Met Lys Lys Phe Asp Gln Thr Gly Pro Ile Val Arg Trp Leu Thr		1200
	1205	1210
Asp Gln Asn Phe Tyr Gly Glu Thr Tyr Gly Gln Thr Gln Ala Thr Val		1215
	1220	1225
Met Ala Phe Gln Ala Leu Ala Glu Tyr Glu Ile Gln Met Pro Thr His		1230
	1235	1240
Lys Asp Leu Asn Leu Asp Ile Thr Ile Glu Leu Pro Asp Arg Glu Val		1245
1250	1255	1260
Pro Ile Arg Tyr Arg Ile Asn Tyr Glu Asn Ala Leu Leu Ala Arg Thr		1265
1265	1270	1275
Val Glu Thr Lys Leu Asn Gln Asp Ile Thr Val Thr Ala Ser Gly Asp		1280
	1285	1290
Gly Lys Ala Thr Met Thr Ile Leu Thr Phe Tyr Asn Ala Gln Leu Gln		1295
	1300	1305
Glu Lys Ala Asn Val Cys Asn Lys Phe His Leu Asn Val Ser Val Glu		1310
	1315	1320
Asn Ile His Leu Asn Ala Met Gly Ala Lys Gly Ala Leu Met Leu Lys		1325
	1330	1335
Ile Cys Thr Arg Tyr Leu Gly Glu Val Asp Ser Thr Met Thr Ile Ile		1340
1345	1350	1355
Asp Ile Ser Met Leu Thr Gly Phe Leu Pro Asp Ala Glu Asp Leu Thr		1360
	1365	1370
Arg Leu Ser Lys Gly Val Asp Arg Tyr Ile Ser Arg Tyr Glu Val Asp		1375
	1380	1385
Asn Asn Met Ala Gln Lys Val Ala Val Ile Ile Tyr Leu Asn Lys Val		1390
	1395	1400
Ser His Ser Glu Asp Glu Cys Leu His Phe Lys Ile Leu Lys His Phe		1405
1410	1415	1420
Glu Val Gly Phe Ile Gln Pro Gly Ser Val Lys Val Tyr Ser Tyr Tyr		1425
1425	1430	1435
Asn Leu Asp Glu Lys Cys Thr Lys Phe Tyr His Pro Asp Lys Gly Thr		1440
	1445	1450
Gly Leu Leu Asn Lys Ile Cys Ile Gly Asn Val Cys Arg Cys Ala Gly		1455
	1460	1465
Glu Thr Cys Ser Ser Leu Asn His Gln Glu Arg Ile Asp Val Pro Leu		1470
	1475	1480
Gln Ile Glu Lys Ala Cys Glu Thr Asn Val Asp Tyr Val Tyr Lys Thr		1485

1490		1495		1500
Lys Leu Leu Arg Ile Glu Glu Gln Asp Gly Asn Asp Ile Tyr Val Met				
1505		1510		1515
Asp Val Leu Glu Val Ile Lys Gln Gly Thr Asp Glu Asn Pro Arg Ala				1520
	1525		1530	1535
Lys Thr His Gln Tyr Ile Ser Gln Arg Lys Cys Gln Glu Ala Leu Asn				
	1540		1545	1550
Leu Lys Val Asn Asp Asp Tyr Leu Ile Trp Gly Ser Arg Ser Asp Leu				
	1555		1560	1565
Leu Pro Thr Lys Asp Lys Ile Ser Tyr Ile Ile Thr Lys Asn Thr Trp				
	1570		1575	1580
Ile Glu Arg Trp Pro His Glu Asp Glu Cys Gln Glu Glu Glu Phe Gln				
1585		1590		1595
Lys Leu Cys Asp Asp Phe Ala Gln Phe Ser Tyr Thr Leu Thr Glu Phe				1600
	1605		1610	1615
Gly Cys Pro Thr				
	1620			

<210> 25
 <211> 3039
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

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 aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataa acctgctcct 180
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<210> 26

<211> 1033

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 26

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Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg
      35          40          45
Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu
      50          55          60
Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro
65          70          75          80
Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val
          85          90          95
Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp
          100         105         110
Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys
          115         120         125
Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro
          130         135         140
Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile
145          150         155         160
His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly
          165         170         175
Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu
          180         185         190
Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro
          195         200         205
Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly
          210         215         220
Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe
225          230         235         240
Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys

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Glu	Ile	Phe	Cys	Pro	Ser	Pro	Pro	Pro	Pro	Ile	Leu	Asn	Gly	Arg	His	Ile		
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Gly	Asn	Ser	Leu	Ala	Asn	Val	Ser	Tyr	Gly	Ser	Ile	Val	Thr	Tyr	Thr			
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Cys	Asp	Pro	Asp	Pro	Glu	Glu	Gly	Val	Asn	Phe	Ile	Leu	Ile	Gly	Glu			
305					310					315					320			
Ser	Thr	Leu	Arg	Cys	Thr	Val	Asp	Ser	Gln	Lys	Thr	Gly	Thr	Trp	Ser			
				325					330					335				
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		340						345					350					
His	Pro	Gln	Ile	Leu	Arg	Gly	Arg	Met	Val	Ser	Gly	Gln	Lys	Asp	Arg			
		355				360						365						
Tyr	Thr	Tyr	Asn	Asp	Thr	Val	Ile	Phe	Ala	Cys	Met	Phe	Gly	Phe	Thr			
		370				375					380							
Leu	Lys	Gly	Ser	Lys	Gln	Ile	Arg	Cys	Asn	Ala	Gln	Gly	Thr	Trp	Glu			
385					390					395					400			
Pro	Ser	Ala	Pro	Val	Cys	Glu	Lys	Glu	Cys	Gln	Ala	Pro	Pro	Asn	Ile			
				405					410					415				
Leu	Asn	Gly	Gln	Lys	Glu	Asp	Arg	His	Met	Val	Arg	Phe	Asp	Pro	Gly			
			420					425					430					
Thr	Ser	Ile	Lys	Tyr	Ser	Cys	Asn	Pro	Gly	Tyr	Val	Leu	Val	Gly	Glu			
		435				440						445						
Glu	Ser	Ile	Gln	Cys	Thr	Ser	Glu	Gly	Val	Trp	Thr	Pro	Pro	Val	Pro			
		450				455					460							
Gln	Cys	Lys	Val	Ala	Ala	Cys	Glu	Ala	Thr	Gly	Arg	Gln	Leu	Leu	Thr			
465					470					475					480			
Lys	Pro	Gln	His	Gln	Phe	Val	Arg	Pro	Asp	Val	Asn	Ser	Ser	Cys	Gly			
				485					490					495				
Glu	Gly	Tyr	Lys	Leu	Ser	Gly	Ser	Val	Tyr	Gln	Glu	Cys	Gln	Gly	Thr			
			500					505					510					
Ile	Pro	Trp	Phe	Met	Glu	Ile	Arg	Leu	Cys	Lys	Glu	Ile	Thr	Cys	Pro			
		515					520					525						
Pro	Pro	Pro	Val	Ile	Tyr	Asn	Gly	Ala	His	Thr	Gly	Ser	Ser	Leu	Glu			
		530				535					540							
Asp	Phe	Pro	Tyr	Gly	Thr	Val	Thr	Tyr	Thr	Cys	Asn	Pro	Gly	Pro				
545					550					555				560				
Glu	Arg	Gly	Val	Glu	Phe	Ser	Leu	Ile	Gly	Glu	Ser	Thr	Ile	Arg	Cys			
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Thr	Ser	Asn	Asp	Gln	Glu	Arg	Gly	Thr	Trp	Ser	Gly	Pro	Ala	Pro	Leu			
				580				585					590					
Cys	Lys	Leu	Ser	Leu	Leu	Ala	Val	Gln	Cys	Ser	His	Val	His	Ile	Ala			
		595				600						605						
Asn	Gly	Tyr	Lys	Ile	Ser	Gly	Lys	Glu	Ala	Pro	Tyr	Phe	Tyr	Asn	Asp			
		610				615						620						
Thr	Val	Thr	Phe	Lys	Cys	Tyr	Ser	Gly	Phe	Thr	Leu	Lys	Gly	Ser	Ser			
625					630					635					640			
Gln	Ile	Arg	Cys	Lys	Ala	Asp	Asn	Thr	Trp	Asp	Pro	Glu	Ile	Pro	Val			
				645					650					655				
Cys	Glu	Lys	Glu	Thr	Cys	Gln	His	Val	Arg	Gln	Ser	Leu	Gln	Glu	Leu			
			660					665					670					
Pro	Ala	Gly	Ser	Arg	Val	Glu	Leu	Val	Asn	Thr	Ser	Cys	Gln	Asp	Gly			
		675				680						685						
Tyr	Gln	Leu	Thr	Gly	His	Ala	Tyr	Gln	Met	Cys	Gln	Asp	Ala	Glu	Asn			
		690				695					700							
Gly	Ile	Trp	Phe	Lys	Lys	Ile	Pro	Leu	Cys	Lys	Val	Ile	His	Cys	His			
705					710					715				720				
Pro	Pro	Pro	Val	Ile	Val	Asn	Gly	Lys	His	Thr	Gly	Met	Met	Ala	Glu			
				725					730					735				

Asn	Phe	Leu	Tyr	Gly	Asn	Glu	Val	Ser	Tyr	Glu	Cys	Asp	Gln	Gly	Phe	
		740						745					750			
Tyr	Leu	Leu	Gly	Glu	Lys	Lys	Leu	Gln	Cys	Arg	Ser	Asp	Ser	Lys	Gly	
		755					760					765				
His	Gly	Ser	Trp	Ser	Gly	Pro	Ser	Pro	Gln	Cys	Leu	Arg	Ser	Pro	Pro	
		770				775						780				
Val	Thr	Arg	Cys	Pro	Asn	Pro	Glu	Val	Lys	His	Gly	Tyr	Lys	Leu	Asn	
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Lys	Thr	His	Ser	Ala	Tyr	Ser	His	Asn	Asp	Ile	Val	Tyr	Val	Asp	Cys	
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Asn	Pro	Gly	Phe	Ile	Met	Asn	Gly	Ser	Arg	Val	Ile	Arg	Cys	His	Thr	
		820						825					830			
Asp	Asn	Thr	Trp	Val	Pro	Gly	Val	Pro	Thr	Cys	Met	Lys	Lys	Ala	Phe	
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Ile	Gly	Cys	Pro	Pro	Pro	Pro	Lys	Thr	Pro	Asn	Gly	Asn	His	Thr	Gly	
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Gly	Asn	Ile	Ala	Arg	Phe	Ser	Pro	Gly	Met	Ser	Ile	Leu	Tyr	Ser	Cys	
				870					875						880	
Asp	Gln	Gly	Tyr	Leu	Leu	Val	Gly	Glu	Ala	Leu	Leu	Leu	Cys	Thr	His	
			885					890							895	
Glu	Gly	Thr	Trp	Ser	Gln	Pro	Ala	Pro	His	Cys	Lys	Glu	Val	Asn	Cys	
		900						905					910			
Ser	Ser	Pro	Ala	Asp	Met	Asp	Gly	Ile	Gln	Lys	Gly	Leu	Glu	Pro	Arg	
		915					920					925				
Lys	Met	Tyr	Gln	Tyr	Gly	Ala	Val	Val	Thr	Leu	Glu	Cys	Glu	Asp	Gly	
		930			935						940					
Tyr	Met	Leu	Glu	Gly	Ser	Pro	Gln	Ser	Gln	Cys	Gln	Ser	Asp	His	Gln	
		945			950					955					960	
Trp	Asn	Pro	Pro	Leu	Ala	Val	Cys	Arg	Ser	Arg	Ser	Leu	Ala	Pro	Val	
			965					970							975	
Leu	Cys	Gly	Ile	Ala	Ala	Gly	Leu	Ile	Leu	Leu	Thr	Phe	Leu	Ile	Val	
		980						985					990			
Ile	Thr	Leu	Tyr	Val	Ile	Ser	Lys	His	Arg	Glu	Arg	Asn	Tyr	Tyr	Thr	
		995				1000						1005				
Asp	Thr	Ser	Gln	Lys	Glu	Ala	Phe	His	Leu	Glu	Ala	Arg	Glu	Val	Tyr	
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Ser	Val	Asp	Pro	Tyr	Asn	Pro	Ala	Ser								
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<210> 27

<211> 3042

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 27

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tcaggagact gggatggtgt catcccgaca tgcaaagagg cccagtgtga acatccagga 600
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<210> 28

<211> 1014

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 28

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Pro Ser Tyr Arg Leu Ile Gly Glu Lys Ala Ile Phe Cys Ile Ser Glu
      35             40             45
Asn Gln Val His Ala Thr Trp Asp Lys Ala Pro Pro Ile Cys Glu Ser
      50             55             60
Val Asn Lys Thr Ile Ser Cys Ser Asp Pro Ile Val Pro Gly Gly Phe

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			100					105					110	Trp
Cys	Gln	Ala	Asn	Glu	Met	Trp	Gly	Pro	Thr	Ala	Leu	Pro	Val	Cys
			115				120					125		Glu
Ser	Asp	Phe	Pro	Leu	Glu	Cys	Pro	Ser	Leu	Pro	Thr	Ile	His	Asn
			130			135					140			Gly
His	His	Thr	Gly	Gln	His	Val	Asp	Gln	Phe	Val	Ala	Gly	Leu	Ser
145					150					155				160
Thr	Tyr	Ser	Cys	Glu	Pro	Gly	Tyr	Leu	Leu	Thr	Gly	Lys	Lys	Thr
			165					170						175
Lys	Cys	Leu	Ser	Ser	Gly	Asp	Trp	Asp	Gly	Val	Ile	Pro	Thr	Cys
			180				185					190		Lys
Glu	Ala	Gln	Cys	Glu	His	Pro	Gly	Lys	Phe	Pro	Asn	Gly	Gln	Val
			195				200					205		Lys
Glu	Pro	Leu	Ser	Leu	Gln	Val	Gly	Thr	Thr	Val	Tyr	Phe	Ser	Cys
			210			215					220			Asn
Glu	Gly	Tyr	Gln	Leu	Gln	Gly	Gln	Pro	Ser	Ser	Gln	Cys	Val	Ile
225					230					235				240
Glu	Gln	Lys	Ala	Ile	Trp	Thr	Lys	Lys	Pro	Val	Cys	Lys	Glu	Ile
			245					250						255
Cys	Pro	Pro	Pro	Pro	Pro	Val	Arg	Asn	Gly	Ser	His	Thr	Gly	Ser
			260				265					270		Phe
Ser	Glu	Asn	Val	Pro	Tyr	Gly	Ser	Thr	Val	Thr	Tyr	Thr	Cys	Asp
			275			280					285			Pro
Ser	Pro	Glu	Lys	Gly	Val	Ser	Phe	Thr	Leu	Ile	Gly	Glu	Lys	Thr
			290			295					300			Ile
Asn	Cys	Thr	Thr	Gly	Ser	Gln	Lys	Thr	Gly	Ile	Trp	Ser	Gly	Pro
305					310					315				320
Pro	Tyr	Cys	Val	Leu	Ser	Thr	Ser	Ala	Val	Leu	Cys	Leu	Gln	Pro
			325					330						335
Ile	Lys	Arg	Gly	Gln	Ile	Leu	Ser	Ile	Leu	Lys	Asp	Ser	Tyr	Ser
			340					345				350		Tyr
Asn	Asp	Thr	Val	Ala	Phe	Ser	Cys	Glu	Pro	Gly	Phe	Thr	Leu	Lys
			355			360					365			Gly
Asn	Arg	Ser	Ile	Arg	Cys	Asn	Ala	His	Gly	Thr	Trp	Glu	Pro	Pro
			370			375					380			Val
Pro	Val	Cys	Glu	Lys	Gly	Cys	Gln	Ala	Pro	Pro	Lys	Ile	Ile	Asn
385					390				395					400
Gln	Lys	Glu	Asp	Ser	Tyr	Leu	Leu	Asn	Phe	Asp	Pro	Gly	Thr	Ser
			405					410						415
Arg	Tyr	Ser	Cys	Asp	Pro	Gly	Tyr	Leu	Leu	Val	Gly	Glu	Asp	Thr
			420				425					430		Ile
His	Cys	Thr	Pro	Glu	Gly	Lys	Trp	Thr	Pro	Ile	Thr	Pro	Gln	Cys
			435			440					445			Thr
Val	Ala	Glu	Cys	Lys	Pro	Val	Gly	Pro	His	Leu	Phe	Lys	Arg	Pro
			450			455				460				Gln
Asn	Gln	Phe	Ile	Arg	Thr	Ala	Val	Asn	Ser	Ser	Cys	Asp	Glu	Gly
465					470				475					480
Gln	Leu	Ser	Glu	Ser	Ala	Tyr	Gln	Leu	Cys	Gln	Gly	Thr	Ile	Pro
			485					490						495
Phe	Ile	Glu	Ile	Arg	Leu	Cys	Lys	Glu	Ile	Thr	Cys	Pro	Pro	Pro
			500				505					510		Pro
Val	Ile	His	Asn	Gly	Thr	His	Thr	Trp	Ser	Ser	Ser	Glu	Asp	Val
			515			520						525		Pro
Tyr	Gly	Thr	Val	Val	Thr	Tyr	Met	Cys	Tyr	Pro	Gly	Pro	Glu	Glu
			530			535					540			Gly
Val	Lys	Phe	Lys	Leu	Ile	Gly	Glu	Gln	Thr	Ile	His	Cys	Thr	Ser
545					550					555				560

Ser Arg Gly Arg Gly Ser Trp Ser Ser Pro Ala Pro Leu Cys Lys Leu
 565 570 575
 Ser Leu Pro Ala Val Gln Cys Thr Asp Val His Val Glu Asn Gly Val
 580 585 590
 Lys Leu Thr Asp Asn Lys Ala Pro Tyr Phe Tyr Asn Asp Ser Val Met
 595 600 605
 Phe Lys Cys Asp Asp Gly Tyr Ile Leu Ser Gly Ser Ser Gln Ile Arg
 610 615 620
 Cys Lys Ala Asn Asn Thr Trp Asp Pro Glu Lys Pro Leu Cys Lys Lys
 625 630 635 640
 Glu Gly Cys Glu Pro Met Arg Val His Gly Leu Pro Asp Asp Ser His
 645 650 655
 Ile Lys Leu Val Lys Arg Thr Cys Gln Asn Gly Tyr Gln Leu Thr Gly
 660 665 670
 Tyr Thr Tyr Glu Lys Cys Gln Asn Ala Glu Asn Gly Thr Trp Phe Lys
 675 680 685
 Lys Ile Glu Val Cys Thr Val Ile Leu Cys Gln Pro Pro Pro Lys Ile
 690 695 700
 Ala Asn Gly Gly His Thr Gly Met Met Ala Lys His Phe Leu Tyr Gly
 705 710 715 720
 Asn Glu Val Ser Tyr Glu Cys Asp Glu Gly Phe Tyr Leu Leu Gly Glu
 725 730 735
 Lys Ser Leu Gln Cys Val Asn Asp Ser Lys Gly His Gly Ser Trp Ser
 740 745 750
 Gly Pro Pro Pro Gln Cys Leu Gln Ser Ser Pro Leu Thr His Cys Pro
 755 760 765
 Asp Pro Glu Val Lys His Gly Tyr Lys Leu Asn Lys Thr His Ser Ala
 770 775 780
 Phe Ser His Asn Asp Ile Val His Phe Val Cys Asn Gln Gly Phe Ile
 785 790 795 800
 Met Asn Gly Ser His Leu Ile Arg Cys His Thr Asn Asn Thr Trp Leu
 805 810 815
 Pro Gly Val Pro Thr Cys Ile Arg Lys Ala Ser Leu Gly Cys Gln Ser
 820 825 830
 Pro Ser Thr Ile Pro Asn Gly Asn His Thr Gly Gly Ser Ile Ala Arg
 835 840 845
 Phe Pro Pro Gly Met Ser Val Met Tyr Ser Cys Tyr Gln Gly Phe Leu
 850 855 860
 Met Ala Gly Glu Ala Arg Leu Ile Cys Thr His Glu Gly Thr Trp Ser
 865 870 875 880
 Gln Pro Pro Pro Phe Cys Lys Glu Val Asn Cys Ser Phe Pro Glu Asp
 885 890 895
 Thr Asn Gly Ile Gln Lys Gly Phe Gln Pro Gly Lys Thr Tyr Arg Phe
 900 905 910
 Gly Ala Thr Val Thr Leu Glu Cys Glu Asp Gly Tyr Thr Leu Glu Gly
 915 920 925
 Ser Pro Gln Ser Gln Cys Gln Asp Asp Ser Gln Trp Asn Pro Pro Leu
 930 935 940
 Ala Leu Cys Lys Tyr Arg Arg Trp Ser Thr Ile Pro Leu Ile Cys Gly
 945 950 955 960
 Ile Ser Val Gly Ser Ala Leu Ile Ile Leu Met Ser Val Gly Phe Cys
 965 970 975
 Met Ile Leu Lys His Arg Glu Ser Asn Tyr Tyr Thr Lys Thr Arg Pro
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 Lys Glu Gly Ala Leu His Leu Glu Thr Arg Glu Val Tyr Ser Ile Asp
 995 1000 1005
 Pro Tyr Asn Pro Ala Ser
 1010

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<211> 1033
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

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 Gly Val Leu Gly Ile Ser Cys Gly Ser Pro Pro Pro Val Leu Asn Gly
 20 25 30
 Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg
 35 40 45
 Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu
 50 55 60
 Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro
 65 70 75 80
 Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val
 85 90 95
 Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp
 100 105 110
 Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys
 115 120 125
 Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro
 130 135 140
 Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile
 145 150 155 160
 His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly
 165 170 175
 Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu
 180 185 190
 Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro
 195 200 205
 Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly
 210 215 220
 Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe
 225 230 235 240
 Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys
 245 250 255
 Val Ile Ala Gly Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu
 260 265 270
 Glu Ile Phe Cys Pro Ser Pro Pro Pro Ile Leu Asn Gly Arg His Ile
 275 280 285
 Gly Asn Ser Leu Ala Asn Val Ser Tyr Gly Ser Ile Val Thr Tyr Thr
 290 295 300
 Cys Asp Pro Asp Pro Glu Glu Gly Val Asn Phe Ile Leu Ile Gly Glu
 305 310 315 320
 Ser Thr Leu Arg Cys Thr Val Asp Ser Gln Lys Thr Gly Thr Trp Ser
 325 330 335
 Gly Pro Ala Pro Arg Cys Glu Leu Ser Thr Ser Ala Val Gln Cys Pro
 340 345 350
 His Pro Gln Ile Leu Arg Gly Arg Met Val Ser Gly Gln Lys Asp Arg
 355 360 365
 Tyr Thr Tyr Asn Asp Thr Val Ile Phe Ala Cys Met Phe Gly Phe Thr
 370 375 380
 Leu Lys Gly Ser Lys Gln Ile Arg Cys Asn Ala Gln Gly Thr Trp Glu
 385 390 395 400
 Pro Ser Ala Pro Val Cys Glu Lys Glu Cys Gln Ala Pro Pro Asn Ile
 405 410 415

Leu	Asn	Gly	Gln	Lys	Glu	Asp	Arg	His	Met	Val	Arg	Phe	Asp	Pro	Gly
			420					425					430		
Thr	Ser	Ile	Lys	Tyr	Ser	Cys	Asn	Pro	Gly	Tyr	Val	Leu	Val	Gly	Glu
		435					440					445			
Glu	Ser	Ile	Gln	Cys	Thr	Ser	Glu	Gly	Val	Trp	Thr	Pro	Pro	Val	Pro
		450				455				460					
Gln	Cys	Lys	Val	Ala	Ala	Cys	Glu	Ala	Thr	Gly	Arg	Gln	Leu	Leu	Thr
465				470						475					480
Lys	Pro	Gln	His	Gln	Phe	Val	Arg	Pro	Asp	Val	Asn	Ser	Ser	Cys	Gly
			485					490						495	
Glu	Gly	Tyr	Lys	Leu	Ser	Gly	Ser	Val	Tyr	Gln	Glu	Cys	Gln	Gly	Thr
			500				505					510			
Ile	Pro	Trp	Phe	Met	Glu	Ile	Arg	Leu	Cys	Lys	Glu	Ile	Thr	Cys	Pro
		515					520				525				
Pro	Pro	Pro	Val	Ile	Tyr	Asn	Gly	Ala	His	Thr	Gly	Ser	Ser	Leu	Glu
		530				535					540				
Asp	Phe	Pro	Tyr	Gly	Thr	Thr	Val	Thr	Tyr	Thr	Cys	Asn	Pro	Gly	Pro
545				550						555					560
Glu	Arg	Gly	Val	Glu	Phe	Ser	Leu	Ile	Gly	Glu	Ser	Thr	Ile	Arg	Cys
			565					570					575		
Thr	Ser	Asn	Asp	Gln	Glu	Arg	Gly	Thr	Trp	Ser	Gly	Pro	Ala	Pro	Leu
			580				585					590			
Cys	Lys	Leu	Ser	Leu	Leu	Ala	Val	Gln	Cys	Ser	His	Val	His	Ile	Ala
		595				600					605				
Asn	Gly	Tyr	Lys	Ile	Ser	Gly	Lys	Glu	Ala	Pro	Tyr	Phe	Tyr	Asn	Asp
		610				615					620				
Thr	Val	Thr	Phe	Lys	Cys	Tyr	Ser	Gly	Phe	Thr	Leu	Lys	Gly	Ser	Ser
625				630						635					640
Gln	Ile	Arg	Cys	Lys	Ala	Asp	Asn	Thr	Trp	Asp	Pro	Glu	Ile	Pro	Val
			645					650				655			
Cys	Glu	Lys	Glu	Thr	Cys	Gln	His	Val	Arg	Gln	Ser	Leu	Gln	Glu	Leu
			660				665					670			
Pro	Ala	Gly	Ser	Arg	Val	Glu	Leu	Val	Asn	Thr	Ser	Cys	Gln	Asp	Gly
		675				680					685				
Tyr	Gln	Leu	Thr	Gly	His	Ala	Tyr	Gln	Met	Cys	Gln	Asp	Ala	Glu	Asn
		690				695				700					
Gly	Ile	Trp	Phe	Lys	Lys	Ile	Pro	Leu	Cys	Lys	Val	Ile	His	Cys	His
705				710						715					720
Pro	Pro	Pro	Val	Ile	Val	Asn	Gly	Lys	His	Thr	Gly	Met	Met	Ala	Glu
			725					730				735			
Asn	Phe	Leu	Tyr	Gly	Asn	Glu	Val	Ser	Tyr	Glu	Cys	Asp	Gln	Gly	Phe
			740			745					750				
Tyr	Leu	Leu	Gly	Glu	Lys	Lys	Leu	Gln	Cys	Arg	Ser	Asp	Ser	Lys	Gly
		755				760				765					
His	Gly	Ser	Trp	Ser	Gly	Pro	Ser								

